

FIG. 1A

CACGAGGGAG CGCTAACGTC TTTCTGTCTC CCCGCGGTGG TG ATG ACG GTG AAA 54
Met Thr Val Lys
1

ACT GAG GCT GCT AAG GGC ACC CTC ACT TAC TCC AGG ATG AGG GGC ATG 102
Thr Glu Ala Ala Lys Gly Thr Leu Thr Tyr Ser Arg Met Arg Gly Met
5 10 15 20

GTG GCA ATT CTC ATC GCT TTC ATG AAG CAG AGG AGG ATG GGT CTG AAC 150
Val Ala Ile Leu Ile Ala Phe Met Lys Gln Arg Arg Met Gly Leu Asn
25 30 35

GAC TTT ATT CAG AAG ATT GCC AAT AAC TCC TAT GCA TGC AAA CAC CCT 198
Asp Phe Ile Gln Lys Ile Ala Asn Asn Ser Tyr Ala Cys Lys His Pro
40 45 50

GAA GTT CAG TCC ATC TTG AAG ATC TCC CAA CCT CAG GAG CCT GAG CTT 246
Glu Val Gln Ser Ile Leu Lys Ile Ser Gln Pro Gln Glu Pro Glu Leu
55 60 65

ATG AAT GCC AAC CCT TCT CCT CCA CCA AGT CCT TCT CAG CAA ATC AAC 294
Met Asn Ala Asn Pro Ser Pro Pro Pro Ser Pro Ser Gln Gln Ile Asn
70 75 80

CTT GGC CCG TCG TCC AAT CCT CAT GCT AAA CCA TCT GAC TTT CAC TTC 342
Leu Gly Pro Ser Ser Asn Pro His Ala Lys Pro Ser Asp Phe His Phe
85 90 95 100

FIG. 1B

TTG AAA GTG ATC GGA AAG GGC AGT TTT GGA AAG GTT CTT CTA GCA AGA 390
Leu Lys Val Ile Gly Lys Gly Ser Phe Gly Lys Val Leu Leu Ala Arg
105 110 115

CAC AAG GCA GAA GAA GTG TTC TAT GCA GTC AAA GTT TTA CAG AAG AAA 438
His Lys Ala Glu Glu Val Phe Tyr Ala Val Lys Val Leu Gln Lys Lys
120 125 130

GCA ATC CTG AAA AAG AAA GAG GAG AAG CAT ATT ATG TCG GAG CGG AAT 486
Ala Ile Leu Lys Lys Lys Glu Glu Lys His Ile Met Ser Glu Arg Asn
135 140 145

GTT CTG TTG AAG AAT GTG AAG CAC CCT TTC CTG GTG GGC CTT CAC TTC 534
Val Leu Leu Lys Asn Val Lys His Pro Phe Leu Val Gly Leu His Phe
150 155 160

TCT TTC CAG ACT GCT GAC AAA TTG TAC TTT GTC CTA GAC TAC ATT AAT 582
Ser Phe Gln Thr Ala Asp Lys Leu Tyr Phe Val Leu Asp Tyr Ile Asn
165 170 175 180

GGT GGA GAG TTG TTC TAC CAT CTC CAG AGG GAA CGC TGC TTC CTG GAA 630
Gly Gly Glu Leu Phe Tyr His Leu Gln Arg Glu Arg Cys Phe Leu Glu
185 190 195

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ATT CTG AAC AAG CCT CTC CAG CTG AAA CCA AAT ATT ACA AAT TCC GCA 1014
Ile Leu Asn Lys Pro Leu Gln Leu Lys Pro Asn Ile Thr Asn Ser Ala
310 315 320

Title: CELL VOLUME-
REGULATED HUMAN KINASE H-
SGK

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FIG. 1D

AGA CAC CTC CTG GAG GGC CTC CTG CAG AAG GAC AGG ACA AAG CGG CTC 1062
Arg His Leu Leu Glu Gly Leu Leu Gln Lys Asp Arg Thr Lys Arg Leu
325 330 335 340

GGG GCC AAG GAT GAC TTC ATG GAG ATT AAG AGT CAT GTC TTC TTC TCC 1110
Gly Ala Lys Asp Asp Phe Met Glu Ile Lys Ser His Val Phe Phe Ser
345 350 355

TTA ATT AAC TGG GAT GAT CTC ATT AAT AAG AAG ATT ACT CCC CCT TTT 1158
Leu Ile Asn Trp Asp Asp Leu Ile Asn Lys Lys Ile Thr Pro Pro Phe
360 365 370

AAC CCA AAT GTG AGT GGG CCC AAC GAG CTA CGG CAC TTT GAC CCC GAG 1206
Asn Pro Asn Val Ser Gly Pro Asn Glu Leu Arg His Phe Asp Pro Glu
375 380 385

TTT ACC GAA GAG CCT GTC CCC AAC TCC ATT GGC AAG TCC CCT GAC AGC 1254
Phe Thr Glu Glu Pro Val Pro Asn Ser Ile Gly Lys Ser Pro Asp Ser
390 395 400

GTC CTC GTC ACA GCC AGC GTC AAG GAA GCT GCC GAG GCT TTC CTA GGC 1302
Val Leu Val Thr Ala Ser Val Lys Glu Ala Ala Glu Ala Phe Leu Gly
405 410 415 420

TTT TCC TAT GCG CCT CCC ACG GAC TCT TTC CTC TGAACCCTGT TAGGGCTTGG 1355
Phe Ser Tyr Ala Pro Pro Thr Asp Ser Phe Leu
425 430

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TTTTAAAGGA	TTTATGTGT	GTTTCCGAAT	GTTTLAGTTA	GCCTTTTGGT	GGAGCCGCCA	1415
GCTGACAGGA	CATCTTACAA	GAGAATTTGC	ACATCTCTGG	AAGCTTAGCA	ATCTTATTGC	1475
ACACTGTTCG	CTGGAATTTT	TTGAAGAGCA	CATTCTCCTC	AGTGAGCTCA	TGAGGTTTTC	1535
ATTTTTATTTC	TTCCTTCCAA	CGTGGTGCTA	TCTCTGAAAC	GAGCGTTAGA	GTGCCGCCTT	1595
AGACGGAGGC	AGGAGTTTCG	TTAGAAAGCG	GACCTGTTCT	AAAAAAGGTC	TCCTGCAGAT	1655
CTGTCTGGGC	TGTGATGACG	AATATTATGA	AATGTGCCTT	TTCTGAAGAG	ATTGTGTTAG	1715
CTCCAAAGCT	TTTCCTATCG	CAGTGTTTCA	GTTCTTTATT	TTCCCTTG TG	GATATGCTGT	1775
GTGAACCGTC	GTGTGAGTGT	GGTATGCCTG	ATCACAGATG	GATTTTGTTA	TAAGCATCAA	1835
TGTGACACTT	GCAGGACACT	ACAACGTGGG	ACATTGTTTG	TTTCTTCCAT	ATTTGGAAGA	1895
TAAATTTATG	TGTAGACTTT	TTTGTAAGAT	ACGGTTAATA	ACTAAAATTT	ATTGAAATGG	1955
TCTTGCAATG	ACTCGTATTC	AGATGCCTAA	AGAAAGCATT	GCTGCTACAA	ATATTTCTAT	2015
TTTTAGAAAG	GGTTTTTATG	GACCAATGCC	CCAGTTGTCA	GTCAGAGCCG	TTGGTGTTTT	2075
TCATTGTTTA	AAATGTCACC	TGTAAAATGG	GCATTATTTA	TGTTTTTTTT	TTTGCAATCC	2135
TGATAATTGT	ATGTATTGTA	TAAAGAACGT	CTGTACATTG	GGTTATAACA	CTAGTATATT	2195
TAAACTTACA	GGCTTATTTG	TAATGTAAAC	CACCATTTTA	ATGTACTGTA	ATTAACATGG	2255
TTATAATACG	TACAATCCTT	CCCTCATCCC	ATCACACAAC	TTTTTTTG TG	TGTGATAAAC	2315
TGATTTTGGT	TTGCAATAAA	ACCTTGAAAA	ATAAAAAAAA	AAAAAAAAAA	AAAAA	2370

THE

Leu Gln Lys Lys Ala Ile Leu Lys Lys Lys Glu Glu Lys His Ile Met
130 135 140

FIG. 2B

Ser Glu Arg Asn Val Leu Leu Lys Asn Val Lys His Pro Phe Leu Val
145 150 155 160

Gly Leu His Phe Ser Phe Gln Thr Ala Asp Lys Leu Tyr Phe Val Leu
165 170 175

Asp Tyr Ile Asn Gly Gly Glu Leu Phe Tyr His Leu Gln Arg Glu Arg
180 185 190

Cys Phe Leu Glu Pro Arg Ala Arg Phe Tyr Ala Ala Glu Ile Ala Ser
195 200 205

Ala Leu Gly Tyr Leu His Ser Leu Asn Ile Val Tyr Arg Asp Leu Lys
210 215 220

Pro Glu Asn Ile Leu Leu Asp Ser Gln Gly His Ile Val Leu Thr Asp
225 230 235 240

Phe Gly Leu Cys Lys Glu Asn Ile Glu His Asn Ser Thr Thr Ser Thr
245 250 255

Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu His Lys Gln
260 265 270

Pro Tyr Asp Arg Thr Val Asp Trp Trp Cys Leu Gly Ala Val Leu Tyr
275 280 285

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FIG. 2C

Glu Met Leu Tyr Gly Leu Pro Pro Phe Tyr Ser Arg Asn Thr Ala Glu
290 295 300

Met Tyr Asp Asn Ile Leu Asn Lys Pro Leu Gln Leu Lys Pro Asn Ile
305 310 315 320

Thr Asn Ser Ala Arg His Leu Leu Glu Gly Leu Leu Gln Lys Asp Arg
325 330 335

Thr Lys Arg Leu Gly Ala Lys Asp Asp Phe Met Glu Ile Lys Ser His
340 345 350

Val Phe Phe Ser Leu Ile Asn Trp Asp Asp Leu Ile Asn Lys Lys Ile
355 360 365

Thr Pro Pro Phe Asn Pro Asn Val Ser Gly Pro Asn Glu Leu Arg His
370 375 380

Phe Asp Pro Glu Phe Thr Glu Glu Pro Val Pro Asn Ser Ile Gly Lys
385 390 395 400

Ser Pro Asp Ser Val Leu Val Thr Ala Ser Val Lys Glu Ala Ala Glu
405 410 415

Ala Phe Leu Gly Phe Ser Tyr Ala Pro Pro Thr Asp Ser Phe Leu
420 425 430

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